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NGBI BLAST Search Results

BLAST Entrez ?

BLASTN 2.1.1 [Aug-8-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 971791677-8991-23542

Query=

(17 letters)

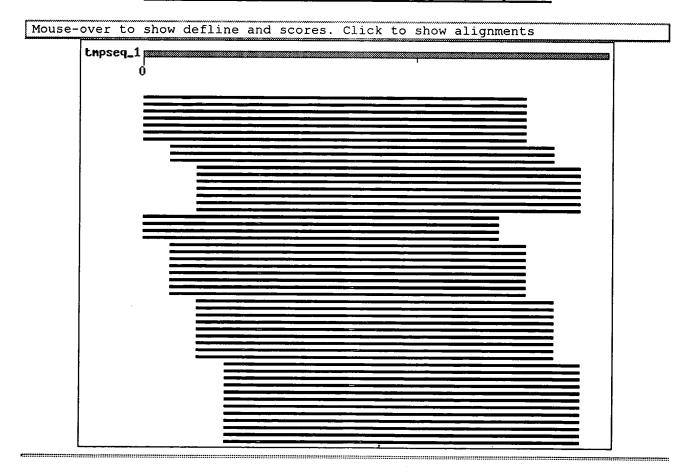
Database: nt

709,140 sequences; 2,366,395,475 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 66 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Sco (bi	re ts)	E Value
gb AC003653.2 AE003653 gb AC009890.12 AC009890 gb AC005099.1 AC005099 gb AC005548.1 AC005548 emb AL365229.13 AL365229 Drosophila melanogaster genomic scaf Genomic Sequence For Homo sapiens C Homo sapiens BAC clone CTA-351J1 fro Homo sapiens chromosome 17, clone hR	30 30 30 30 30	1.9 1.9 1.9 1.9	
gb AF022794.1 AF022794 Homo sapiens chromosome 21q22.2 cosm gb AF020800.1 AF020800 Homo sapiens cosmid Q96E10 from the emb AL138831.12 AL138831 Human DNA sequence from clone RP3 gb U80460.1 HSXIST2 Human Xq13 3' end of PAC 92E23 containi	30 30 30	1.9 1.9 1.9	
emb AL163267.2 HS21C067 gb AF016420.1 CELC13D9 Homo sapiens chromosome 21 segment emb AJ229042.1 HS229042 Homo sapiens 959 kb contig between emb AL024498.12 HS417M14 Human DNA sequence from clone RP3	30 30 30 30 30	1.9 1.9 1.9	
emb AL121578.1 HSXKSRPXR emb AJ248285.1 CNSPAX03 Pyrococcus abyssi complete genome; dbj AB023039.1 AB023039 Arabidopsis thaliana genomic DNA, c gb M35878.1 HUMIBP3 Human insulin-like growth factor-bindin	30 30 30 30	1.9 1.9 1.9 1.9	
gb U18839.1 SCE9747 Saccharomyces cerevisiae chromosome V c gb AE003442.1 AE003442 Drosophila melanogaster genomic scaf gb AE003600.2 AE003600 Drosophila melanogaster genomic scaf gb AC005283.2 AC005283 Homo sapiens PAC clone RP5-1039L24 f	28 28 28 28	7.4 7.4 7.4 7.4	
gb AC074283.2 AC074283 gb AC008639.7 AC008639 gb AC016644.7 AC016644 gb AF121105.1 AF121105 Homo sapiens chromosome 10 clone OSJ Homo sapiens chromosome 5 clone RP11 Homo sapiens interleukin 16 gene, pa	28 28 28 28 28	7.4 7.4 7.4 7.4	
ref NC 001137.2 Saccharomyces cerevisiae chromosome V, com gb AC009075.6 AC009075 Homo sapiens chromosome 16 clone RP1 gb AF244084.1 AF244084 Edwardsiella ictaluri plasmid pEI2, gb AE002176.2 AE002176 Chlamydophila pneumoniae AR39, secti	28 28 28 28	7.4 7.4 7.4 7.4	
gb AF254983.1 AF254983 Homo sapiens chromosome 21 clone BAC gb AC003078.1 AC003078 Human BAC clone GS1-117010 from 7q21 ref NM 007584.1 Mus musculus cell adhesion kinase (Cak), mRNA gb AC004682.1 HUAC004682 Homo sapiens Chromosome 16 BAC clo	28 28 28 28	7.4 7.4 7.4 7.4	
gb AC007207.22 AC007207 Homo sapiens 12p13.3-4.6-10.5 BAC R ref NC 001778.1 Polypterus ornatipinnis mitochondrion, com gb AE001644.1 AE001644 Chlamydia pneumoniae section 60 of 1 gb AC006287.1 AC006287 Homo sapiens, clone hRPK.22 A 1, com	28 28 28 28	7.4 7.4 7.4 7.4	
gb AC003019.1 AC003019 gb AC005888.1 AC005888 Homo sapiens 12q24.2 PAC RPCI1-116K2 gb AC005808.1 AC005808 Homo sapiens chromosome 20, P1 clone gb U62532.1 POU62532 Polypterus ornatipinnis complete mitoc	28 28 28 28	7.4 7.4 7.4 7.4	
gb AC002366.1 AC002366 Human Xp22 BAC CT-285115 (from CalTe emb AL139087.13 AL139087 Human DNA sequence from clone RP11 emb AL137067.7 AL137067 Human DNA sequence from clone RP4 emb AL1578167.15 D1158167 Human DNA sequence from clone RP11	28 28 28 28	7.4 7.4 7.4	
emb AL158167.15 AL158167 emb AX012403.1 AX012403 emb AL163201.2 HS21C001 emb AL158043.14 AL158043 gb AF026259.1 AF026259 Human DNA sequence from clone RP11 Human DNA sequence from clone RP11 Human DNA sequence from clone RP11	28 28 28 28	7.4 7.4 7.4	
emb AL118508.27 HSJ737E23 Human DNA sequence from clone RP4 emb AL161669.3 CNS01RHC Human chromosome 14 DNA sequence ** emb AL135747.2 CNS01DVE Human chromosome 14 DNA sequence **	28 28 28 28	7.4 7.4 7.4	
emb AL133241.3 CNS01DUE	28 28 28 28	7.4 7.4 7.4	
emb AL078476.2 HSB7L1C4 Homo sapiens chromosome 21 BAC B7L1 dbj AP002547.2 AP002547 Chlamydophila pneumoniae genomic DN	28 28 28	7.4 7.4 7.4	

Sequences producing significant alignments:	Sco: (bi		E Value
gb AE003653.2 AE003653 gb AC009890.12 AC009890 gb AC005099.1 AC005099 Homo sapiens BAC clone CTA-351J1 fro	30	1.9	
gb AC005548.1 AC005548 Homo sapiens chromosome 17, clone hR	30	1.9	
emb AL365229.13 AL365229 Human DNA sequence from clone RP11 gb AF022794.1 AF022794 Homo sapiens chromosome 21q22.2 cosm	30	1.9 1.9	
gb AF020800.1 AF020800 Homo sapiens cosmid Q96E10 from the	30	1.9	
gb U80460.1 HSXIST2 Human Xq13 3' end of PAC 92E23 containi	<u>30</u> 30	1.9	
emb AL163267.2 HS21C067 Homo sapiens chromosome 21 segment gb AF016420.1 CELC13D9 Caenorhabditis elegans cosmid C13D9	30	1.9	
emb AJ229042.1 HS229042 Homo sapiens 959 kb contig between	30	1.9 1.9	
emb AL024498.12 HS417M14 Human DNA sequence from clone RP3 emb AL121578.1 HSXKSRPXR Homo sapiens chromosome X sequence	30	1.9 1.9	
<pre>emb AJ248285.1 CNSPAX03</pre> Pyrococcus abyssi complete genome;	30	1.9	
<pre>dbj AB023039.1 AB023039 Arabidopsis thaliana genomic DNA, c gb M35878.1 HUMIBP3 Human insulin-like growth factor-bindin</pre>	<u>30</u> 30	1.9 1.9	
gb U18839.1 SCE9747 Saccharomyces cerevisiae chromosome V c	28	7.4	
gb AE003442.1 AE003442 Drosophila melanogaster genomic scaf gb AE003600.2 AE003600 Drosophila melanogaster genomic scaf	<u>28</u> 28	7.4 7.4	
gb AC005283.2 AC005283 Homo sapiens PAC clone RP5-1039L24 f	28	7.4	
gb AC074283.2 AC074283 Oryza sativa chromosome 10 clone OSJ gb AC008639.7 AC008639 Homo sapiens chromosome 5 clone CTB	<u>28</u> 28	7.4 7.4	
gb AC016644.7 AC016644 Homo sapiens chromosome 5 clone RP11	28	7.4	
gb AF121105.1 AF121105 Homo sapiens interleukin 16 gene, pa ref NC 001137.2 Saccharomyces cerevisiae chromosome V, com	$\frac{28}{28}$	7.4 7.4	
gb AC009075.6 AC009075 Homo sapiens chromosome 16 clone RP1 gb AF244084.1 AF244084 Edwardsiella ictaluri plasmid pEI2,	28	7.4 7.4	
gb AE002176.2 AE002176 Chlamydophila pneumoniae AR39, secti	28	7.4	
gb AF254983.1 AF254983 Homo sapiens chromosome 21 clone BAC gb AC003078.1 AC003078 Human BAC clone GS1-117010 from 7q21	28	7.4 7.4	
ref[NM 007584.1] Mus musculus cell adhesion kinase (Cak), mRNA	28	7.4	
gb AC004682.1 HUAC004682	28	7.4 7.4	
ref NC 001778.1 Polypterus ornatipinnis mitochondrion, com	28	7.4	
gb AE001644.1 AE001644 Chlamydia pneumoniae section 60 of 1 gb AC006287.1 AC006287 Homo sapiens, clone hRPK.22_A_1, com	28	7.4 7.4	
gb AC003019.1 AC003019 Mus musculus Chromosome 4 BAC clone	28	7.4	
gb AC005888.1 AC005888	<u>28</u> 28	7.4 7.4	
gb U62532.1 POU62532 Polypterus ornatipinnis complete mitoc	28	7.4	
emb AL139087.13 AL139087 Human DNA sequence from clone RP11		7.4 7.4	
emb AL157838.24 AL157838 Human DNA sequence from clone RP4 emb AL137067.7 AL137067 Human DNA sequence from clone RP11		7.4	
emb AL158167.15 AL158167 Human DNA sequence from clone RP11		7.4 7.4	
<pre>emb AX012403.1 AX012403 emb AL163201.2 HS21C001 Homo sapiens chromosome 21 segment</pre>		7.4 7.4	
emb AL158043.14 AL158043 Human DNA sequence from clone RP11		7.4	
gb AF026259.1 AF026259 Mus musculus receptor-like tyrosine emb AL118508.27 HSJ737E23 Human DNA sequence from clone RP4		7.4 7.4	
emb AL161669.3 CNS01RHC Human chromosome 14 DNA sequence **	28	7.4	
emb AL135747.2 CNS01DVE Human chromosome 14 DNA sequence ** emb AL133241.3 CNS01DUE Human chromosome 14 DNA sequence **		7.4 7.4	
emb AL162755.2 NMA4Z2491 Neisseria meningitidis serogroup A	28	7.4	
gb L07554.1 LINPEROX Linum usitatissimum peroxidase (FLXPER emb AL033397.7 HS27K12 Human DNA sequence from clone 27K12		7.4 7.4	
emb AL023655.1 HS242N11 Human DNA sequence from clone 242N1	28	7.4	
<pre>emb AL078476.2 HSB7L1C4 dbj AP002547.2 AP002547</pre> Homo sapiens chromosome 21 BAC B7L1 Chlamydophila pneumoniae genomic DN		7.4 7.4	

```
gb|L57509.1|MUSCAK Mus musculus Cak receptor kinase mRNA, c...
                                                                              7.4
dbj|AB026898.1|AB026898 Homo sapiens DNA, DLEC1 to ORCTL4 g...
                                                                          28
                                                                              7.4
dbj|D64000.1|SYCSLRB Synechocystis sp. PCC6803 complete gen... emb|Y10466.1|SOPRXR5 S.oleracea mRNA for peroxidase, clone ...
                                                                          28
                                                                              7.4
                                                                          28
                                                                              7.4
dbj|AP000499.1|AP000499 Homo sapiens genomic DNA, chromosom...
                                                                              7.4
                                                                          28
gb|L26525.1|RATPTK3D Rattus norvegicus tyrosine kinase rece...
                                                                              7.4
                                       Alignments
>gb|AE003653.2|AE003653 Drosophila melanogaster genomic scaffold 142000013386055 :
             of 63, complete sequence
           Length = 249469
 Score = 30.2 \text{ bits } (15), \text{ Expect} = 1.9
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 Strand = Plus / Plus
Query: 2
             aattaggatggggaa 16
             11111111111111
Sbjct: 2445 aattaggatggggaa 2459
>gb|AC009890.12|AC009890 Genomic Sequence For Homo sapiens Clone H_NH0262L04 From
               complete sequence
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
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               111111111111111
Sbjct: 142165 gaattaggatgggga 142151
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
Query: 3
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              1111111111111
Sbjct: 70042 attaggatggggaaa 70028
>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756_K_11, complete
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 Identities = 15/15 (100%)
 Strand = Plus / Plus
Query: 1
               gaattaggatgggga 15
               Sbjct: 133477 gaattaggatgggga 133491
>emb|AL365229.13|AL365229 Human DNA sequence from clone RP11-723K16 on chromosome
              sequence [Homo sapiens]
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 Identities = 15/15 (100%)
```

```
gb|L57509.1|MUSCAK Mus musculus Cak receptor kinase mRNA, c...
                                                                         7.4
dbj|AB026898.1|AB026898 Homo sapiens DNA, DLEC1 to ORCTL4 g...
                                                                     28
                                                                         7.4
dbj|D64000.1|SYCSLRB Synechocystis sp. PCC6803 complete gen... emb|Y10466.1|SOPRXR5 S.oleracea mRNA for peroxidase, clone ...
                                                                     28
                                                                         7.4
                                                                     28
                                                                         7.4
dbj|AP000499.1|AP000499 Homo sapiens genomic DNA, chromosom...
                                                                         7.4
                                                                     28
gb|L26525.1|RATPTK3D Rattus norvegicus tyrosine kinase rece...
                                                                         7.4
                                     Alignments
>gb|AE003653.2|AE003653 Drosophila melanogaster genomic scaffold 142000013386055:
            of 63, complete sequence
          Length = 249469
 Score = 30.2 bits (15), Expect = 1.9
 Identities = 15/15 (100%)
 Strand = Plus / Plus
Query: 2
            aattaggatggggaa 16
            Sbjct: 2445 aattaggatggggaa 2459
>gb|AC009890.12|AC009890 Genomic Sequence For Homo sapiens Clone H NH0262L04 From
              complete sequence
          Length = 177223
 Score = 30.2 bits (15), Expect = 1.9
 Identities = 15/15 (100%)
 Strand = Plus / Minus
Query: 1
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              11111111111111
Sbjct: 142165 gaattaggatgggga 142151
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          Length = 131611
 Score = 30.2 bits (15), Expect = 1.9
 Identities = 15/15 \cdot (100\%)
 Strand = Plus / Minus
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             Sbjct: 70042 attaggatggggaaa 70028
>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756 K 11, complete
          Length = 156811
Score = 30.2 \text{ bits } (15), \text{ Expect} = 1.9
 Identities = 15/15 (100%)
Strand = Plus / Plus
Query: 1
              gaattaggatgggga 15
              Sbjct: 133477 gaattaggatgggga 133491
>emb|AL365229.13|AL365229 Human DNA sequence from clone RP11-723K16 on chromosome
             sequence [Homo sapiens]
          Length = 121478
Score = 30.2 bits (15), Expect = 1.9
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Identities = 15/15 (100%)

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Strand = Plus / Plus
Query: 1
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             11111111111111
Sbjct: 58988 gaattaggatgggga 59002
>gb|AF022794.1|AF022794 Homo sapiens chromosome 21q22.2 cosmid Q80D10, complete se
          Length = 44897
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 Strand = Plus / Minus
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             Sbjct: 14979 attaggatggggaaa 14965
>gb|AF020800.1|AF020800 Homo sapiens cosmid Q96E10 from the Down Syndrome critica:
             chromosome 21q22.2, complete sequence
          Length = 41075
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
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             Sbjct: 39162 attaggatggggaaa 39148
>emb|AL138831.12|AL138831 Human DNA sequence from clone RP3-406P24 on chromosome (
             sequence [Homo sapiens]
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
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             1111111111111
Sbjct: 17231 gaattaggatgggga 17217
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Identities = 15/15 (100%)
Strand = Plus / Plus
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Sbjct: 36978 aattaggatggggaa 36992
>emb|AL163267.2|HS21C067 Homo sapiens chromosome 21 segment HS21C067
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Score = 30.2 bits (15), Expect = 1.9
Identities = 15/15 (100%)
Strand = Plus / Plus
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Strand = Plus / Plus
Query: 1
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              11111111111111
Sbjct: 58988 gaattaggatgggga 59002
>gb|AF022794.1|AF022794 Homo sapiens chromosome 21q22.2 cosmid Q80D10, complete se
          Length = 44897
 Score = 30.2 \text{ bits (15)}, Expect = 1.9
 Identities = 15/15 (100%)
 Strand = Plus / Minus
Query: 3
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             1111111111111
Sbjct: 14979 attaggatggggaaa 14965
>gb|AF020800.1|AF020800 Homo sapiens cosmid Q96E10 from the Down Syndrome critical
             chromosome 21q22.2, complete sequence
          Length = 41075
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
Query: 3
             attaggatggggaaa 17
             11111111111111
Sbjct: 39162 attaggatggggaaa 39148
>emb|AL138831.12|AL138831 Human DNA sequence from clone RP3-406P24 on chromosome (
             sequence [Homo sapiens]
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 Identities = 15/15 (100%)
 Strand = Plus / Minus
Query: 1
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             11111111111111
Sbjct: 17231 gaattaggatgggga 17217
>gb|U80460.1|HSXIST2 Human Xq13 3' end of PAC 92E23 containing the X inactivation
             (XIST) gene, complete sequence [Homo sapiens]
          Length = 135886
 Score = 30.2 bits (15), Expect = 1.9
 Identities = 15/15 (100%)
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Query: 2
             aattaggatggggaa 16
             1111111111111
Sbjct: 36978 aattaggatggggaa 36992
>emb|AL163267.2|HS21C067 Homo sapiens chromosome 21 segment HS21C067
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Score = 30.2 \text{ bits (15)}, Expect = 1.9
Identities = 15/15 (100%)
Strand = Plus / Plus
```

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Query: 3
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              1111111111111111
Sbjct: 253757 attaggatggggaaa 253771
>gb|AF016420.1|CELC13D9 Caenorhabditis elegans cosmid C13D9
          Length = 43487
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Query: 1
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             1111111111111
Sbjct: 24516 gaattaggatgggga 24530
>emb|AJ229042.1|HS229042 Homo sapiens 959 kb contig between AML1 and CBR1 on chror
              segment 2/3
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              Sbjct: 284320 attaggatggggaaa 284306
>emb|AL024498.12|HS417M14 Human DNA sequence from clone RP3-417M14 on chromosome (
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             serine/threonine-protein kinase (ortholog of mouse and rat
             MAK (male germ cell-associated kinase), the 3' end of the
             GCMB gene for glial cells>
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Sbjct: 79114 attaggatggggaaa 79100
>emb|AL121578.1|HSXKSRPXR Homo sapiens chromosome X sequence from 12 cosmids, map
             DXS709-SRPX, complete sequence
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 Strand = Plus / Minus
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             11111111111
Sbjct: 40278 attaggatggggaaa 40264
>emb|AJ248285.1|CNSPAX03 Pyrococcus abyssi complete genome; segment 3/6
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Strand = Plus / Minus
```

```
Query: 3
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             1111111111111111
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>emb|AJ229042.1|HS229042 Homo sapiens 959 kb contig between AML1 and CBR1 on chror
              segment 2/3
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              111111111111
Sbjct: 284320 attaggatggggaaa 284306
>emb|AL024\underline{498.12}|HS417M14 Human DNA sequence from clone RP3-417M14 on chromosome (
             Contains a novel gene, the gene for a novel
             serine/threonine-protein kinase (ortholog of mouse and rat
             MAK (male germ cell-associated kinase), the 3' end of the
             GCMB gene for glial cells>
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>emb|AL121578.1|HSXKSRPXR Homo sapiens chromosome X sequence from 12 cosmids, map
            DXS709-SRPX, complete sequence
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             Sbjct: 40278 attaggatggggaaa 40264
>emb|AJ248285.1|CNSPAX03 Pyrococcus abyssi complete genome; segment 3/6
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Score = 30.2 bits (15), Expect = 1.9
Identities = 15/15 (100%)
Strand = Plus / Minus
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